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gtttaatggg tttggggaga tgcagggatc actgcaatgt ggatgaaaaa gagatacaga	540
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tgcaatatgg aacaccaaat gtacttaatg aagacgtcca agaaatgcta aaacctgcca	660
agaattetag tgetgtgata caaagaaaac atattttate tgtteteece caaatcaaaa	720
gcactagett ttttgetaat accaactttg teatcattee aaatgeeace eetatgaact	780
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gtaacaccaa agaaagcaga gattctgcca ctgcctcgcc accaccagca ccacctccac	900
caaacatact gccaacacca tcactggagc tagaggaagc agaagagcag taatgtggat	960
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catcctaaaa	gcaaataatt	actctatcat	ctacgtgccc	tttgcttctt	aaagttactc	240
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cagcctgccc	atttgccttc	atcaacattc	ctaaacactg	ggcttaaaat	gtagtatgag	360
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gtg aac aca gaa ttt att ggc ttg aga cgc tgt tta atg ggt ttg ggg Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly 20 25 30	96
aga tgc agg gat cac tgc aat gtg gat gaa aaa gag ata cag aaa tgc Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys 35 40 45	144
aag atg aaa aaa tgt tgt gtt gga cca aaa gtg gtt aaa ttg att aaa Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys 50 55 60	192
aac tac ctg caa tat gga aca cca aat gta ctt aat gaa gac gtc caa Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln 65 70 75 80	240
gaa atg cta aaa cct gcc aag aat tct agt gct gtg ata caa aga aaa Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys 85 90 95	288
cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt gct His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala 100 105 110	336
aat acc aac ttt gtc atc att cca aat gcc acc cct atg aac tct gcc Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala 115 120 125	384
acc atc agc act atg acc cca gga cag atc aca tac act gct act tct Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser 130 135 140	432
acc aag agt aac acc aaa gaa agc aga gat tot goc act goc tog cca Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro 145 150 155 160	480
cca cca gca cca cct cca cca aac ata ctg cca aca cca tca ctg gag Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu 165 170 175	528
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Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln

Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys

His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala 100

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala 120 115

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser 130 135

Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro 155 160 145 150

Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu 165 170

Leu Glu Glu Ala Glu Glu Gln 180

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<212> DNA

<213> Homo sapiens

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aga Arg	tgc Cys	agg Arg 35	gat Asp	cac His	tgc Cys	aat Asn	gtg Val 40	gat Asp	gaa Glu	aaa Lys	gag Glu	ata Ile 45	cag Gln	aaa Lys	tgc Cys	144
		aaa Lys														192
		cta Leu														240
		cta Leu														288
cat His	att Ile	tta Leu	tct Ser 100	gtt Val	ctc Leu	ccc Pro	caa Gln	atc Ile 105	aaa Lys	agc Ser	act Thr	agc Ser	ttt Phe 110	ttt Phe	gct Ala	336
		aac Asn 115														384
		agc Ser														432
		agt Ser														480
cca Pro	cca Pro	gca Ala	cca Pro	cct Pro 165	cca Pro	cca Pro	aac Asn	ata Ile	ctg Leu 170	cca Pro	aca Thr	cca Pro	tca Ser	ctg Leu 175	gag Glu	528
		gaa Glu	_	-		_	taa									552
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Arg Cys Arg Asp Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys 50 55 60

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln 65 70 75 80

Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys 85 90 95

His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala 100 105 110

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala 115 120 125

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser 130 135 140

Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro 145 150 155 160

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Leu Glu Glu Ala Glu Glu Gln 180

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<223> Coding sequence for the variant human DEFB118 gene

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96

gtg atc cca gcc tat agt ggt gaa aaa aaa tgc tgg aac aga tca ggg

Val Ile Pro	Ala Tyr 20	Ser	Gly	Glu	Lys 25	Lys	Cys	Trp	Asn	Arg 30	Ser	Gly	
cac cgc agg His Arg Arg 35													144
aaa aat ctt Lys Asn Leu 50	cga gct Arg Ala	tgc Cys	tgc Cys 55	att Ile	cca Pro	tcc Ser	aat Asn	gaa Glu 60	gac Asp	cac His	agg Arg	cga Arg	192
gtt cct gcg Val Pro Ala 65	aca tct Thr Ser	ccc Pro 70	aca Thr	ccc Pro	ttg Leu	agt Ser	gac Asp 75	tca Ser	aca Thr	cca Pro	gga Gly	att Ile 80	240
att gat gat Ile Asp Asp	att tta Ile Leu 85	aca Thr	gta Val	agg Arg	ttc Phe	acg Thr 90	aca Thr	gac Asp	tac Tyr	ttt Phe	gaa Glu 95	gta Val	288
agc agc aag Ser Ser Lys	aaa gat Lys Asp 100	atg Met	gtt Val	gaa Glu	gag Glu 105	tct Ser	gag Glu	gcg Ala	gga Gly	agg Arg 110	gga Gly	act Thr	336
gag acc tct Glu Thr Ser 115								tga					372
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Glu Thr Ser Leu Pro Asn Val His His Ser Ser 115 120	
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cac tgc agg aaa caa tgc aaa gat gga gaa gca gtg aaa gat aca tgc His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys 35 40 45	144
aaa aat ctt cga gct tgc tgc att cca tcc aat gaa gac cac agg cga Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg 50 55 60	192
gtt cct gcg aca tct ccc aca ccc ttg agt gac tca aca cca gga att Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile 65 70 75 80	240
att gat gat att tta aca gta agg ttc acg aca gac tac ttt gaa gta Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val 85 90 95	288
agc agc aag aaa gat atg gtt gaa gag tct gag gcg gga agg gga act Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr 100 105 110	336
gag acc tct ctt cca aat gtt cac cat agc tca tga Glu Thr Ser Leu Pro Asn Val His His Ser Ser 115 120	372
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Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly 20 25 30	

His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys 35 40 Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg 55 50 Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile 75 70 Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val 85 90 Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr 100 105 Glu Thr Ser Leu Pro Asn Val His His Ser Ser 115 120 <210> 45 <211> 20 <212> DNA <213> Artificial Sequence <220> <223> PCR primer <400> 45 20 aggttgagta tttgccagac <210> 46 <211> 19 <212> DNA <213> Artificial Sequence <220> <223> PCR primer <400> 46 19 aggacagggg tgagtgata <210> 47 <211> 246 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(246)<223> Coding sequence for the variant human DEFB126 gene 48 atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln 10 ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga 96 Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 25 30

									4	∠ -T						
att Ile	tgc Cys	aag Lys 35	aag Lys	aag Lys	tgc Cys	aaa Lys	cct Pro 40	gaa Glu	gag Glu	atg Met	cat His	gta Val 45	aag Lys	aat Asn	ggt Gly	144
		atg Met														192
		atc Ile														240
cag Gln	taa															246
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Leu	Val	Ser	Gly 20	Asn	Trp	Tyr	Val	Lys 25	Lys	Cys	Leu	Asn	Asp 30	Val	Gly	
Ile	Cys	Lys 35	Lys	Lys	Суз	Lys	Pro 40	Glu	Glu	Met	His	Val 45	Lys	Asn	Gly	
Trp	Ala 50	Met	Cys	Gly	Lys	Gly 55	Thr	Ala	Val	Phe	Gln 60	Leu	Thr	Asp	Val	
Leu 65	Ile	Ile	Leu	Phe	Ser 70	Val	Ser	Arg	Gln	Arg 75	Leu	Gln	Glu	Phe	Gln 80	
Gln																
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Leu Val	Ser	Gly 20	Asn	Trp	Tyr	Val	Lys 25	Lys	Cys	Leu	Asn	Asp 30	Val	Gly	
att tgc Ile Cys	aag Lys 35	aag Lys	aag Lys	tgc Cys	aaa Lys	cct Pro 40	gaa Glu	gag Glu	atg Met	cat His	gta Val 45	aag Lys	aat Asn	ggt Gly	144
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cgt gct Arg Ala 65															240
tca aca Ser Thr															288
gct tcg Ala Ser															336
<211> <212> <213>	50 111 PRT Homo 50	sap:	iens												
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Leu Val	Ser	Gly 20	Asn	Trp	Tyr	Val	Lys 25	Lys	Cys	Leu	Asn	Asp 30	Val	Gly	
Ile Cys	Lys 35	Lys	Lys	Суѕ	Lys	Pro 40	Glu	Glu	Met	His	Val 45 .	Lys	Asn	Gly	
Trp Ala 50	Met	Cys	Gly	Lys	Gln 55	Arg	Asp	Cys	Cys	Val 60	Pro	Ala	Asp	Arg	
Arg Ala 65	Asn	Tyr	Pro	Val 70	Phe	Суз	Val	Gln	Thr 75	Lys	Thr	Thr	Arg	Ile 80	
Ser Thr	Val	Thr	Ala 85	Thr	Thr	Ala	Thr	Thr 90	Thr	Leu	Met	Met	Thr 95	Thr	
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gtage			atgai	ttag												1	8
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ttg g Leu V																9	6
att t Ile C																14	4
tgg g Trp A																192	2
cgt g Arg A 65																240	0
tca a Ser T		_		~							_	_	_			288	3
gct t	.cg	atg	tct	tcg	atg	gct	cct	acc	cgt	ttc	tcc	cac	tgg	ttg	a	334	4

27

Ala Ser Met Ser Ser Met Ala Pro Thr Arg Phe Ser His Trp Leu 100 105 110

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<211> 111

<212> PRT

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Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 20 25 30

Ile Cys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly 35 40 45

Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg 50 55 60

Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile 65 70 75 80

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